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**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicants: Ashkenazi et al. Attorney's Docket No: 39780-2630P1C74

Serial No: 10/020,445 Group Art Unit: 1647

Filed: October 24, 2001 Examiner: Seharaseyon, Jegatheesan

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS  
ENCODING THE SAME**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

**DECLARATION OF AUDREY GODDARD, Ph.D.,**

**PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D.,**

**MARGARET ROY and WILLIAM I. WOOD, Ph.D.**

**UNDER 37 CFR 1.131**

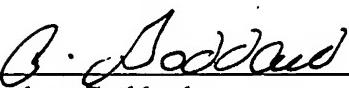
We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Kedra *et al.*, "Homo Sapiens mRNA for Synaptogyrin 2," Accession No. AJ002308, published on March 3, 1998.
3. We conceived and reduced to practice the polypeptide designated as PRO615 (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application in the United States prior to March 3, 1998.
4. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA claimed in the above-identified application that encoded the PRO615 polypeptide (SEQ ID NO: 162).
5. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was, as still is, responsible for overseeing the sequencing of novel

polypeptides, including the PRO615 polypeptide (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application.

6. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was, as still is, responsible for overseeing the homology searches for the novel polypeptides, including that for the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA claimed in the above-identified application.
7. A cDNA clone, referred to as DNA48304-1323 in the above-identified application, was identified as encoding the PRO615 polypeptide.
8. The full length of the cDNA clone is shown in Figure 60 of the above-identified application. The full-length cDNA sequence has 1512 nucleotide residues. The full length of the PRO615 peptide encoded by DNA46804-1323 is shown in Figure 61 of the above-identified application. The full-length PRO615 polypeptide has 224 amino acid residues, and is homologous to human synaptogyrin.
9. Copies of the pages from the GSqEdit database which report the cloning, sequencing and functional data for the PRO615 polypeptide sequence, including its homology to human synaptogyrin, as well as the cloning, sequencing data for the nucleic acid sequence encoding PRO615 are attached to this declaration (with the dates redacted) as Exhibit A.
10. The GSqEdit report shows the full-length nucleic acid sequence for DNA48304-1323 (identified as "DNA48304") and the full-length PRO615 polypeptide encoded by DNA48304. Both the DNA48304 and the PRO615 polypeptide sequences and the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.
11. The DNA48304 sequence shown in the GSqEdit report is identical to that of SEQ ID NO:161 disclosed in the above-identified application.
12. The beginning of the cDNA sequence corresponding to SEQ ID NO:161 in the above-identified application is shown on page 1 of the GSqEdit database report and the location of the first nucleotide is marked with "insert starts here" and an arrow. The

- location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.
13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.
  14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.
  15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.
  16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

  
Audrey Goddard

9/10/04  
Date

Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

Margaret Roy, Ph.D.

Date

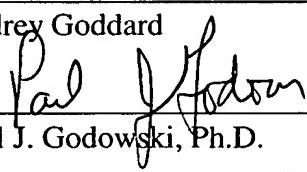
William I. Wood, Ph.D.

Date

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Audrey Goddard



Paul J. Godowski, Ph.D.

Date

9/09/2001

Date

Austin Gurney, Ph.D.

Date

Margaret Roy, Ph.D.

Date

William I. Wood, Ph.D.

Date

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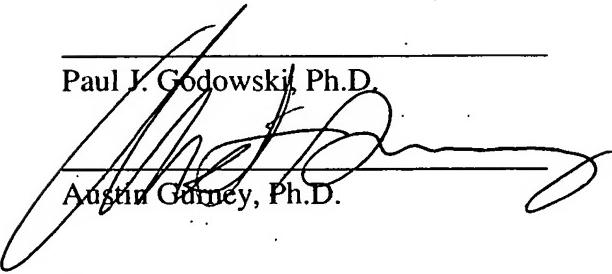
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Audrey Goddard

Date

Paul J. Godowski, Ph.D.

Date

  
Austin Garney, Ph.D.

9/7/04  
Date

Margaret Roy, Ph.D.

Date

William I. Wood, Ph.D.

Date

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Audrey Goddard

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Date

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Paul J. Godowski, Ph.D.

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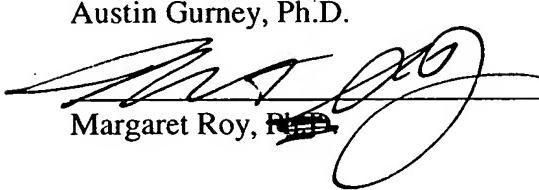
Date

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Austin Gurney, Ph.D.

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Date



Margaret Roy, Ph.D.

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Date

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William I. Wood, Ph.D.

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Date

9/16/04

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Audrey Goddard

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Date

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Paul J. Godowski, Ph.D.

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Date

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Austin Gurney, Ph.D.

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Date

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Margaret Roy, Ph.D.

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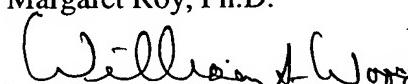
Date

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William I. Wood, Ph.D.

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Date



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9/9/04

>DNA48304 [Full]

>707 Sites [All Sites]

DNA48304 brush GSeqEdit

rmaI  
maeI  
sau3AI  
mboI/ndeII[dam-]  
dpnII[dam-]  
dpnII[dam+]  
alwI[dam-] sau3AI  
tagI sfuI tsp509I[M.ecori-] nlaIV xbaI mboI/ndeII[dam-]  
bstBI mwol haeIII/palI bfaI dpnII[dam-]  
bscI bgII[M.haeIII-] hpy188III tagI  
tfI apoI sfiI eaeI bstYI/xhoII dpnII[dam+]  
hinFI[M.taql-] cfri bamHI[M.mspI-] mnII  
taqI[M.claI-] haeIII/palI alwI[dam-] alwI[dam-]  
bsaJI clai/bsp106 eaeI bsrl mspI[M.bamHI-] [M.haeIII-]  
hpyCH4V bspDI[dam-] cfri tsprI hpalI mnII bstYI/xhoII mnII  
1 TGCACCTCGG TTCTATCGAT TCGAAATTGG CCACACTGGC CGGATCCTCT AGAGATCCCT CGACACTCGAC CCACGGTCC GCGGACGGGT GGGGGACGC  
ACGTGGAGCC AAGATAGCTA AGCTTAAGCC GGTGTACCG GCCTAGGAGA TCTCTAGGGA GCTGGAGCTG GGTGGCAGG CGCCTGGCA CCCGCCTGCG  
† insert starts here







scrFI [dcm-]								
pspGI								
mvaI								
ecoRII [dcm-]								
dsav [dcm-]								
bstNI								
bssKI [dcm-]								
sau3AI								
mboI /ndelII [dam-]	apyI [dcm+]	tsp45I		ddeI [M.aluI-]	bslI			
dpnII [dam-]	sexAI		maeIII	earI/ksp632I		sau96I		
dpnII [dam+]	rsAI		hphI	bspMI	mboII	aluI		
401	tsPRI	aciI	csp6I	bstEI	sapI	bspCN1	hpy188III	
GTATTTCCCC CAGATCAGCA ACGCACTGA CGCGAAGTAC	CTGGTCATTG	GTGACCTGGT	CTTCTCAAGCT	TCCTGGACCT	TCTGTGGT	TGTGGTTTC		
CATAAAGGG GTCTAGTCGT TGGGTGACT GGGGTTCATG	GACCAGTAAC	CACTGGACGA	GAAGAGTCGA	AGGACCTGGA	AGAACACAA	ACAACCAAAG		
91 Y F P - Q I S N A T D R K Y L V I G D L L F S A L W T F L W F V G F								
pleI								
haeIII/pali								
sau96I [M.haeIII-]								
bbvI								
tseI								
pflMI								
hphI	hphI		tail					
bsrI	tsP45I			maeII/hpyCH4IV	mlyI			
mnII	bsII tsPRI	maeIII		nlalV hinfI				
501	TGCTTCTCA CCAACCAGTG	bcgI btrI		TCTGTGAGGG	GGGGGCCGAC			
ACGAAGGAGT GGTTGGTCAC	GGCAGTCACC AACCCGAAGG	ACGTGCTGGT		AGACACTCCC	CTTCAGCTTC	TTTCCATCT		
124 C F L T N Q W A V T N P K D V L V G A D S V R A A I T F S F F S I F		CCGTCACTGG TTGGGCTTC		TGCACGACCA	CCCCGGCTG	GTGGTAGTG	GAAGTCGAAG	AAAAGGTAGA

haeIII/pallI  
 scrFI [dcm-]  
 pspGI  
 mvaI  
 scrFI [dcm-]  
 pspGI  
 mvaI  
 scrFI [dcm-]  
 pspGI  
 mvaI  
 ecoRII [dcm-]  
 dsaV [dcm-]  
 bstNI  
 mnlI bssKI [dcm+]  
 mwoI apyI [dcm-]  
 bgII [M.haeIII-]  
 hinPI  
 sfII [dcm-]  
 bssKI [dcm-]  
 bsajI  
 apyI [dcm+]  
 cac8I  
 haelli/pallI  
 bsajI  
 afel/eco47III  
 haelli  
 cac8I  
 afel/eco47III  
 hincII/hindII avail [M.hpaII-]  
 hincII/hindII avail [M.hpaII-]  
 bsaWI  
 hpy188III tail  
 foki  
 maeII/hpyCH4IV hpaII  
 tspr  
 bstF5I  
 tsp509I  
 bsII  
 accIII  
 btsI  
 tcattcagaa ttacgttgac cccactccgg ACCCCAAACAC  
 AGAGGACCCC ACACCGACCGG AGGGACCCGG A TGGTCCGGAT GTTCGACCG CACCTGGCTGA AGTAGGTCTT AATGCAACTG GGGTGGGCC TGGGGTTGGT  
 601 TCTCCTGGGG TGTGCTGGCC TCCCTGGCCT ACCAGGGCTA CAAGGCTGGC GTGGGACGACT TCATCCAGAA  
 158 S W G V L A S L A Y Q R Y K A G V D D F I Q N Y V D P T P D P N T  
 scrFI [dcm-]  
 pspGI  
 mvaI  
 ecoRII [dcm-]  
 dsaV [dcm-]  
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 bssKI [dcm-]  
 apyI [dcm-]  
 mnII  
 bsajI hpyCH4V  
 hphi  
 bsh1236I  
 bsaji  
 mnII  
 acII  
 rs  
 fnu4HI/bsoFI CS  
 GCCCCCTGTG  
 CGATGGTGG CGATGGTGGT GGAAGTGGGT CTIGCGCCTC TGTTGGCTCC  
 701 TGCCTACGCC TCCTACCCAG GTGCATCTGT GGACAAC TACAGGCCAC CCTTCACCA GAACGCGGAG ACCACCGAGG GCTACAGCC  
 191 A Y A S Y P G A S V D N Y Q Q P P F T Q N A E T T E G Y Q P P V

sau96I [M.haeIII-]  
 haeIII/palI  
 sau96I [M.haeIII-] scrFI [dcm-]  
 pspOMI/bsp120I pspGI  
 nlaIV mvaI  
 eco0109I/draII ecoRII [dcm-]  
 bsp1286 [M.haeIII-]  
 bmyI dsaV [dcm-]  
 banII [M.haeIII-] bstNI  
 apaI bssKI [dcm-]  
 eco0109I/draII apyI [dcm+]  
 ddeI bsmFI mnII mnII bsAJI  
 bspCNI aciI mnII mnII xcmI  
 801 TACTGAGTGG CGGTAGCGT GGGAAAGGGG ACAGAGAGGG CCCTCCCCCTC TGCCCTGGAC TTTCCCATCA GCCTCCTGGA ACTGCCAGGC CCTCTCTTC  
 ATGACTCTACC GCCAATCGCA CCCTTCCCCC TGTCTCTCCC GGGAGGGAG ACGGGACTG AAAGGTAGT CGGAGGACT TGACGGTGG GGAGAGAAAG  
 224 Y O

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scrFI [dcm-]  
 pspGI  
 mvaI aciI  
 ecoRII [dcm-]  
 dsaV [dcm-]  
 bstNI  
 mnII  
 bssKI [dcm-]  
 aluI ddeI [M.aluI-]  
 mspALLI/nspBII mnII  
 tseI mnII  
 fnu4HI/bsoFI mnII  
 bbvI ddeI [M.aluI-]  
 fokI hpyCH4V mnII  
 bstF5I bsgI aluI mnII  
 901 ACCTGTTCA. TCCTGTCAG CTGACACACA GCTAAGGAGC CTCATAGCCT GGCAGAGCCA CACCCAAAGT GGCAGGGCT AGAGGGCTCC  
 TGGACAAGGT AGGACACGTC GACTGTGTG CGATTCTCG GAGTATCGGA CGGGTTCA CGGACACGGG TCTCCCGAAG



scrFI [M.hpaII-]							
ncII							
mspI							
hpII							
xmaI / pspAI							
smaI							
scrFI [M.hpaII-]							
ncII							
sau96I [M.haeIII-]							
mspI [M.haeIII-]							
hpII dsaV							
scrFI [M.hpaII-]							
ncII dsaV							
dsaV bssKI							
bssKI bssKI							
alII							
bslI bslI							
ddEI [M.aluI-] haeIII/palI							
mwoI							
bceAI							
fnu4HI/bsoFI							
pleI							
mlyI							
bspCN I							
bsaJI bsaJI							
haeIII/palI acII							
mlaIV							
mlaIV							
bspMI							
mlaIV							
mlaIV							
cac8I banI							
mlaIV							
1101 GCCAGCAGGT GCCCCATGTGC TACTGACAAG TGCCTAGCT TCCCTGGGGC CCGGTTCAGG CGCTTATTATC TGC GTTCTCT GCCAAAGACT							
CGGTCTGTCCA CGGGTACACG ATGACTGTT ACGGAGTCGA AGGGGGCCG GGCCCAGTCC GGCACCCCTCG GCGATAATAG ACGCAAGAGA CGGTTCTGA							

scrFI [dcm-]  
 pspGI  
 mvaI  
 ecoRII [dcm-]  
 mspAII/nspBII dsav [dcm-]  
 tseI sau96I [dcm-]  
 fnu4HI/bsoFI bstNI mnII  
 bbVI nlaIV avail [dcm-] [M.hpaII-] ddeI  
 sau96I [M.haeIII-] hpyCH4V mspl bssKI [dcm-] econI  
 nlaIV bspMI bsgI acII hpaII apyI [dcm+]  
 1201 CGTGGGGCC ATCACACCTG CCCTGTGCAG CGGAGCCGGAA CCAGGGCTC ACAGGAGTG AGICCAACG AAGGGACAC GGGTACCGAC ATACTAGGCC  
 haeIII/palI  
 sau96I [M.haeIII-] bspMI bspCNII  
 nlaIV  
 1301 GGGCACCOAC CCTGTGCCGG TGGCCTCTGG GCTGCCTCCC TTGGTGTGAG GGGGGGGCTG GTGCTCATGG CACTTCCCTCC TTGCTCCCAC CCCTGGCAGC  
 CCCGGTGGTG GGACACGGCC ACCGGAGACC CGACGGAGGG CACCAACTC CGACGGAGACC  
 nI sau3AI  
 mboI/nde  
 dpnII [da  
 dpnI [dam  
 bsp1286  
 bmyI btsI  
 tseI  
 fnu4HI  
 scrFI [dcm-  
 pspGI  
 mvaI  
 ecoRII [dcm-  
 dsav [dcm-]  
 bstNI  
 dsav [dcm-]  
 bstNI  
 hgiAI/asphi  
 bsp1286  
 bsiHKAI  
 bsII [dcm-] bbvI  
 dsaI  
 tseI btgI/bstDSI  
 mspl mnII fnu4HI/bsoFI  
 draIII hpaII mnII  
 haeIII/palI cfr10I/bsrFI bbVI bsII  
 sau96I [M.haeIII-] haelli/palI mnII acII  
 1301 GGGCACCOAC CCTGTGCCGG TGGCCTCTGG GCTGCCTCCC TTGGTGTGAG GGGGGGGCTG GTGCTCATGG CACTTCCCTCC TTGCTCCCAC CCCTGGCAGC  
 CCCGGTGGTG GGACACGGCC ACCGGAGACC CGACGGAGGG CACCAACTC CGACGGAGACC

scrFI [dcm-]  
 pspGI  
 mvaI  
 tth  
 ecorII [dcm-]  
 dsaV [dcm-]  
 bstNI  
 bssKI [dcm-]  
 bsI [dcm-]  
 bssKI [dcm-]  
 bsp1286  
 mly  
 bmyI dsalI nlaIV alwNI  
 nlaIV btgI/bstDSI hin  
 nlaIV btgI/bstDSI hin  
 apyI [dcm+]  
 banI bsalI alw26  
 sfcI ddeI  
 hpyCH4V  
 pstI maeIII  
 aluI sspl  
 TCCCTTCCCG AACGGAAGGGC TTTGCCTGAC AACACCCAGC TTATATGAAATTATAGACGTC AACATGAAAT CCTTGGACC CCTCCGTCC CCACGGGTA CCGAGGGTCT  
 scrFI [dcm-]  
 pspGI  
 mvaI  
 ecorII [dcm-]  
 dsaV [dcm-]  
 bstNI  
 mwOI  
 haelli/pali  
 mspl [M.haeIII-]  
 scrFI [M.hpaII-]  
 nciI bssKI [dcm-]  
 dsav bsalI sfanI  
 bssKI fokI  
 esp3I  
 bsmBI  
 bsmAI  
 psII  
 sfanI hpaII bstF5I  
 psII apyI [dcm+]  
 GAGACAGACA CGGGCTCACAT ATATTTAG CACCCCTCT ACGGGGCGGA CCCTACGACA AACCTCTGCC TTATTTCAA AAGAGTAAGT TTCTTTTTT  
 1401 AGGGAAAGGGC TTTGCCTGAC AACACCCAGC TTATATGAAATTATAGACGTC AACATGAAAT CCTTGGACC CCTCCGTCC CCACGGGTA CCGAGGGTCT  
 1501 CTCTGTCGT GCCGAGGTGA TTATAAATC GTGGGGGAGA TGGATGCTGT GGGATGGCCGATAAAATGTT TTCTCATCA AAGAAAAAAA  
 →

thaI

fnu4HI/bsoFI

haeIII/palI

mcrI rmaI

eagI/xmaIII/ecclXI

eaEI maeI

cfrI pleI

bsiEI mlyI

notI fnuDII/mvnI

sallI

fnu4HI/bsoFI bfaI

hincII/hindII[M.taqI-]

aciI bstUI xbaI

accI[M.taqI-]

thaI acII hinfI pleI

fnuDII/mvnI hpy188III

bstUI bsh1236I

mlyI

bsh1236I drdI

hinfI[M.taqI-]

TTTTTTTTT TTTGGCGGG CGCTGAGATC TCAGGTGGAC

^prK follows

> length: 1640

accI(GTMKAC) :

accIII(TCCGGA) :

aciI(CCGC) :

afeI(AGGCCT) :

afIII(ACRYGT) :

aluI(AGCT) :

393 1632

686

79 81 93 106 109 115 118 139 153

162 166 182 201 317 335 431 765 789

810 952 1007 1082 1170 1230 1352

1615 1619

634

73 85 97 397

GSeqEdit, DNA48304 [Full], page 12

alw26I (CAGNNNNCTG) :	1497
alwI (GGATCNNNN) :	42 43 54
alwNI (CAGNNNNCTG) :	1497
apaI (GGGCC) :	838
apoI (RAATTY) :	23
apyI (CCWGG) :	368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
asphi (GNGCWC) :	1361
aspI (GACNNNNGTC) :	1499
avaI (CYCGRG) :	1150
avalI (GGWCC) :	475 689 1238
bamHI (GGATCC) :	42
banI (GGYRCC) :	1108 1481
banII (GRGCYC) :	838
bbsI (GAAGACNNNN) :	231
bbvI (GCAGC) :	112 197 570 917 1227 1331 1396
bceAI (ACGGCNNNNNNNNNN) :	124 148 219 1160
bcgI (NNNNNNNNNNNNCGANNNNNNTGCNNNNNNNNNN) :	343 535
bfaI (CTAG) :	49 1048 1095 1627
bgII (GCNNNNNGGC) :	30 334 363 618 987
bmyI (GDGCHC) :	838 985 1022 1109 1278 1361 1482
bpmI (CTGGAG) :	1017
bpuAI (GAAGACNNNNNN) :	231
bsaI (GGTCTCBBBB) :	768
bsaJI (CCNNGG) :	5 79 157 373 604 622 716 775 853 1019 1144 1150 1161 1339 1391 1466
bsaWI (WCCGGW) :	1487 1548
bseRI (GAGGAGNNNNNNNN) :	686
bsgI (GTGCAG) :	1014
bsh1236I (CGCG) :	915 1225
bsiCI (TTCGAA) :	74 80 86 98 152 214 216 398 764 1614 1620

- bsiEI (CGRYCG) :	1616
bsIKAI (GWCWC) :	1361
bsI1 (CCNNNNNNNNGG) :	317 368 478 511 680 758 948 1144 1145 1150 1255 1310 1386 1466 1543
- bsmAI (GTCTC) :	768 1564
bsmAI (GTCTC) :	768 1564
bsmBI (CGTCTCNNNN) :	1564
- bsmFI (GGGAGNNNNNNNNNNNN) :	828
bsOF1 (GCNGC) :	106 109 112 115 118 153 166 182 197 200 334 570 788 917 1006 1169
- bsp106 (ATCGAT) :	15
bsp120I (GGGCC) :	838
bsp1286 (GDGCHC) :	838 985 1022 1109 1278 1361 1482
- bspCNI (CTCAGNNNNNNNNNN) :	464 803 1075 1134 1260
bspDI (ATCGAT) :	15
bspEI (TCCGGA) :	686
bspMI (ACCTGC) :	178 203 454 1105 1216
- bspMII (TCCGGA) :	686
bsrBI (GAGGG) :	137 1007
bsrDI (GCAATGNN) :	277
bsrFI (RCCGGY) :	1316
bsrI (ACTGGN) :	35 515
bssHII (GCGGCC) :	213 215
bssKI (CCNGG) :	368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466
- bssSI (CTCGTG) :	1543 1548
bsstBI (TCGAA) :	285 1199
bstDSI (CCRYGG) :	20
bstEII (GGTNACC) :	79 1161 1339 1487
bstF5I (GGATG) :	450
bstNI (CWGG) :	326 662 909 1552
bstSII (GGATG) :	368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548

bstUI (CGCG) :	74	80	86	98	152	214	216	398	764	1614	1620
bstYI (RGATCY) :	42	53									
btgII (CCAGTGN) :	79	1161	1339	1487							
btrI (CACTC) :	540										
btsI (GCAGTGN) :	343	698	1088	1283							
cac8I (GCNNNGC) :	162	213	215	330	359	614	645	884	958	1084	1101
cfoI (GCC) :	151	185	213	215	217	635					
cfr10I (RCCGGY) :	1316										
cfrI (YGCCCR) :	28	37	154	1616							
clai (ATCGAT) :	15										
csp6I (GTAC) :	302	437	800								
ddeI (CTNAG) :	292	464	803	932	1075	1134	1260	1457			
dpnI (GATC) :	43	54	242	413	1294						
dpnII (GATC) :	43	54	242	413	1294						
draII (RGGNCCY) :	141	837	838								
draIII (CACNNNGTG) :	1308										
drdI (GACNNNNNNTC) :	68	1623									
dsal (CCRYGG) :	79	1161	1339	1487							
dsav (CCNGGG) :	368	440	604	623	717	854	875	948	1019	1145	1150
eaei (YGGCCR) :	1543	1548									
eaigI (CGGCCG) :	28	37	154	1616							
earI (CTCTTCNNNN) :	1616										
ecii (GGCGGA) :	459										
elcIXI (GGGCCG) :	92										
eco47III (AGCGCT) :	1616										
eco57I (CTGAAG) :	634										
ecoli (CTNNNNNAGG) :	581	997									
ecoO109I (RGGNCCY) :	1255										
ecoRI (GAATT) :	141	837	838								

- **ecoriI (CCWGG) :**  
     1564  
     106 109 112 115 118 153 166 182 197 200 334 570 788 917 1006 1169  
     1227 1331 1396 1615 1618  
     74 80 86 98 152 214 216 398 764 1614 1620  
     326 662 909 1552  
     1017  
     184 634  
     29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322  
     1546 1617  
     75 84 96 194 396  
     1361  
     151 185 213 215 217 635  
     151 185 213 215 217 635  
     393 675 1632  
     393 675 1632  
     18 288 558 1197 1499 1623 1630  
     40 687 1146 1151 1236 1317 1544  
     264 450 508 526 577 754 899  
     48 190 472 664 686 1626  
     122 395  
     541 673  
     1 255 722 916 1087 1226 1446  
     459  
     79  
     49 1048 1095 1627  
     541 673  
     451 525 1453  
     43 54 242 413 1294  
     232 382 460 598

**esp3I (CGTCCTC) :**  
**fnu4HI (GCNGC) :**  
**fnuDII (CGCG) :**  
**fokI (GGATG) :**  
**gsuI (CTGGAG) :**  
**haeII (RGGCY) :**  
**haeIII (GGCC) :**  
**hgaI (GACGC) :**  
**hgIAI (GNGCWC) :**  
**hhAI (GCGC) :**  
**hinP1 (GCGC) :**  
**hincII (GTYRAC) :**  
**hindII (GTYRAC) :**  
**hinfI (GANTC) :**  
**hpAII (CCGG) :**  
**hphi (GGTGA) :**  
**hpy188I11 (TCNNGA) :**  
**hpy99I (CGWCG) :**  
**hpyCH4IV (ACGT) :**  
**hpyCH4V (TGCA) :**  
**ksp632I (CTCTTCNNNN) :**  
**kspl (CCCGGG) :**  
**maeI (CTAG) :**  
**maeII (ACGT) :**  
**maeIII (GTNAC) :**  
**mboI (GATC) :**  
**mboII (GAAGA) :**

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mcrI (CGRYCG) :	1616
mluI (ACGCGT) :	73 85 97 397
mlyI (GAGTCNNNN) :	288 558 1197 1499 1623 1630
mnII (CCTC) :	5 46 58 64 267 324 373 506 566 619 709 777 836 842 847 872 891 940
mroI (TCCGGA) :	992 1016 1059 1074 1133 1255 1324 1335 1348 1376 1472 686
mseI (TTAA) :	1067
mslII (CAYNNNNRTG) :	350
mspAII (CMGCKG) :	79 1113 918 1228
mspI (CCGG) :	40 687 1146 1151 1236 1317 1544
mvaI (CCWGG) :	368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548
mvnI (CGCG) :	74 80 86 98 152 214 216 398 764 1614 1620
mwoI (GCNNNNNNNGC) :	30 106 109 112 118 144 153 217 334 363 618 958 987 1079 1160 1182 1547
ncII (CCSGG) :	1145 1150 1151 1543
ncoI (CCATGG) :	1487
ndeII (GATC) :	43 54 242 413 1294
nlaIII (CATG) :	131 1114 1366 1488
nlaIV (GNNCC) :	42 141 168 552 689 838 936 1108 1166 1205 1232 1300 1481 1491 1615
notI (GCGCCGC) :	79 1113 918 1228
nspBII (CMGCKG) :	29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322
pAlI (GGC) :	1546 1617
pf1FI (GACNNNGTC) :	1499
pf1MI (CCANNNNNNTGG) :	511
pleI (GAGTCNNNN) :	288 558 1197 1499 1623 1630
psiI (TTATAA) :	1521
pspAI (CCCGGG) :	1150
pspGI (CCWGG) :	368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548 838
pspOMI (GGGCC) :	838

pstI (CTGGCAG) :	1086	1445
pvuII (CAGCTG) :	918	
rmaI (CTAG) :	49	1048 1095 1627
rsal (GTAC) :	302	437 800
sacII (CCGGGG) :	79	
saiI (GTCGAC) :	393	1632
sapI (GCTCTTCNNNN) :	458	
sau3AI (GATC) :	43	54 242 413 1294
sau96I (GGNCC) :	142	475 553 689 838 839 1148 1206 1238 1301
scrFI (CCNGG) :	368	440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466
	—	1543 1548
sexAI (ACCGGGT) :	439	
sfaNI (GCATC) :	256	327 723 1539 1553
sfcI (CTRYAG) :	272	1086 1445
sfII (GGCCNNNNGCC) :	29	362 617
sfuI (TTCGAA) :	20	
smal (CCCGGG) :	1150	
sspI (AATATT) :	1439	
sstII (CCGGGG) :	79	
styI (CCWWGG) :	157	1487
taiI (ACGT) :	541	673
taqI (TCGA) :	16	21 60 66 175 394 1633
tfII (GAWTC) :	18	
thaI (CGCG) :	74	80 86 98 152 214 216 398 764 1614 1620
	—	1067
tru9I (TTAA) :	112	197 570 917 1227 1331 1396
tseI (GCWGC) :	451	525
tsp45I (GTSAC) :	24	669
tsp509I (AATT) :	34	344 425 516 698 1089 1283
tspRI (NNCAGTGNN) :	1499	
tth111I (GACNNNGTC) :		

xbaI (TCTAGA) :	48	1626
xcmI (CCANNNNNNNNTGG) :	349	865
xhoII (RGATCY) :	42	53
xmaI (CCCGGG) :	1150	
xmaIII (CGGCCCG) :	1616	

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